**Title:** Lineage calling can identify antibiotic resistant clones within minutes

**Abstract:** Surveillance of circulating drug resistant bacteria is essential for healthcare providers to deliver effective empiric antibiotic therapy. However, the results of surveillance may not be available on a timescale that is optimal for guiding patient treatment. Here we present a method for inferring characteristics of an unknown bacterial sample by identifying the presence of sequence variation across the genome that is linked to a phenotype of interest, in this case drug resistance. We demonstrate an implementation of this principle using sequence k-mer content, matched to a database of known genomes. We show this technique can be applied to data from an Oxford Nanopore device in real time and is capable of identifying the presence of a known resistant strain in 5 minutes, even from a complex metagenomic sample. This flexible approach has wide application to pathogen surveillance and may be used to greatly accelerate diagnoses of resistant infections.

**Bio:**
Dr. Karel Břinda's research lies at the intersection of computer science, applied mathematics, biology and epidemiology. He develops methods for rapid prediction of antibiotic resistance from sequencing data and for epidemiological surveillance. Dr. Břinda's previous work focused on resource-frugal methods for sequence data analysis.

Dr. Břinda is a Research Associate in the Harvard Chan School of Public Health and Harvard Medical School. He received PhD in computer science from Université Paris-Est, France. Besides bioinformatics, Dr. Břinda also works on methods for automatic generation of tactile maps for blind users.